

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:34:08 ; Search time 78.57 Seconds
(without alignments)
777,968 Million cell updates/sec

Title: US-09-653-755a-6

Perfect score: 2487
Sequence: 1 EVQLOOSGPELVKPGASVMI.....YIAKTIKSRSPKGGHHHHHH 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTEMBL.16:*
2: sp.archaea:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp.vertibrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1426	57.3	437	11 09RIA4	09ria4 mus musculu
2	547	22.0	416	4 09NPP6	09npp6 homo sapien
3	480.5	19.3	117	11 09QXF0	09qxf0 mus musculu
4	477	19.2	4	09UP60	09up60 homo sapien
5	458.5	18.4	117	11 09QXEX	09qxx9 mus musculu
6	401	16.6	109	11 09UL75	09ul75 mus musculu
7	414	16.1	118	11 0921C4	0921c4 mus musculu
8	385	15.5	114	11 09UL81	09ul81 mus musculu
9	379	15.2	110	11 09UL77	09ul77 mus musculu
10	372.5	15.0	684	13 090544	090544 ginglymosto
11	371.5	14.9	150	4 09Y298	09y298 homo sapien
12	369.5	14.9	4	095978	095978 homo sapien
13	366.5	14.7	119	5 09GY22	09gy22 schistosoma
14	364	14.6	124	4 09UL92	09ul92 homo sapien
15	358.5	14.4	109	11 09UL85	09ul85 mus musculu
16	356	14.3	110	11 09UL83	09ul83 mus musculu
17	353.5	14.2	119	4 09UL94	09ul94 homo sapien
18	349.5	14.1	117	11 0921C6	0921c6 mus musculu
19	348.5	14.0	125	4 09UL95	09ul95 homo sapien

20	328	13.2	116	4 09UL89	09ul89 homo sapien
21	328	13.2	147	4 09Y509	09y509 homo sapien
22	294.5	11.8	119	4 09UL73	09ul73 homo sapien
23	294.5	11.8	298	11 09QXF0	09qxf0 mus musculu
24	284.5	11.4	113	4 09UL90	09ul90 homo sapien
25	284	11.4	118	4 09UL72	09ul72 homo sapien
26	283	11.4	112	4 09HCC1	09hcc1 homo sapien
27	279	11.2	122	4 09UL84	09ul84 homo sapien
28	278	11.2	118	4 09UL91	09ul91 homo sapien
29	277.5	11.2	116	4 09UL93	09ul93 homo sapien
30	270.5	10.9	131	4 09UL88	09ul88 homo sapien
31	268.5	10.8	121	4 09UL71	09ul71 homo sapien
32	266	10.7	4	095973	095973 homo sapien
33	261.5	10.5	102	11 09UL79	09ul79 mus musculu
34	251	10.1	124	6 09N0W6	09n0w6 oryctolagus
35	249	10.0	124	6 09N0W4	09n0w4 oryctolagus
36	243	9.8	122	4 09UL75	09ul75 homo sapien
37	237.5	9.5	104	4 09UL87	09ul87 homo sapien
38	234.5	9.4	121	4 09UL96	09ul96 homo sapien
39	222.5	8.9	112	4 09UGP3	09ugp3 homo sapien
40	212	8.5	95	4 09ULB6	09ulb6 homo sapien
41	189.5	7.6	88	4 075737	075737 homo sapien
42	187	7.5	268	13 090524	090524 ginglymosto
43	182.5	7.3	75	4 075743	075743 homo sapien
44	179	7.2	267	13 090529	090529 ginglymosto
45	176.5	7.1	77	4 075741	075741 homo sapien

ALIGNMENTS

RESULT	1	PREDIMINARY;	PRT;	437 AA.
09RIA4	09RIA4			
AC	09RIA4			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wildie K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;			
RT	"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a			
RT	single chain antibody (scFv).";			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF152372; AAD40243.1; -			
DR	HSSP; P01842; 7FAB.			
DR	InterPro; IPR003600; -			
DR	InterPro; IPR003600; -			
DR	Pfam; PF00047; 1g; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			
DR	SMART; SM00410; IG_Like; 1.			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE	437 AA;	48142 MW;	5C3A7BB3E7D697C CRC64;

Query Match 57.3%; Score 1426; DB 11; Length 437;
Best Local Similarity 60.0%; Pred. No. 2.3e-103;
Matches 275; Conservative 63; Mismatches 94; Indels 26; Gaps 8;

QY	2	VOLDOSGPELVKPGASVMI	SCRTSAYFTENTYVWVQSHSELEMT-----GGINPYG	56
DB	1	VOLDOSGGLVKGSLKLS	CAASGFTFSYAMSVRQTPKRLWASFSGGI-IYTT	59
QY	57	GSISPEKFKRATLVVDKSS	STAYMELSLTSEDNAVYCCARRAGAYFDWGGTTLTV	116
DB	60	DSV-----KGRFTYKDKDR	NIILSIQMSLSRSDTAMTYCAR---GDYSATWGTGLTVT	111

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OY 117 SAKTTPPSVYPLAPGCGDTTGGSSVTLGCLVKYFPESTVTVNNGSLSSVHTFPALLQ 176
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
112 SAKTTPPSVYPLAPGAGTNSMVTGLGCLVKYFPEPTVTVNNGSLSSGVHTFPALLQ 171
OY 177 SGLYTMSSSTVSSSTWPSQOTVTCVAHPASSSTTVDKLEPSCPISTINCPCKECKHC 236
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
172 SDLYTSSSVTVSSSTWPSSTVTCVAHPASSSTTVDKLEPSCPISTINCPCKECKHC 222
OY 237 PAVNLEGSPSVFTFPPKIKVLMISLTPKVTGVVDVSEDDPPVQISMVFNVEVHTAQT 296
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
223 TVEVS---SVFTFPPKPKVLTITLTPKVTGVVDISKDDPEVQISWFDVDEVHTAQT 279
OY 297 QTHREDYNTIRVSTLPIOHODMMSGEKCKCVNNKDLSPLETKISIKIGLVAPQVY 356
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
280 QPREDFNSFRSVSELPIMHODMLNGKEKCKCVNSAFAPIEKTISKTRKRPANQVY 339
OY 357 ILPPAPDLSRKQVSLTCLVGVNPGDISVEMTSNGHTEENYKQFAPVLDSDGSYFIYSK 416
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
340 TTPPKPEOMAKDKVSLTCLMTDFEPEDITVEMQMGPAENYKNTQPIMDTDSYFYYSK 399
OY 417 LNKTKSKMEKTDSESCNVHREGKLNKYKTKTISRSPGK 454
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
400 LNVQKSNMEAGNTFTCSVLHGLHNHTEKNLSHSPGK 437

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RESULT 2

ID Q9NP6 PRELIMINARY: PRT: 416 AA.

AC Q9NP6; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)

DE IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

ON [1]

RP SEQUENCE FROM N.A.

RA Pluvier R., Estivill X., Escarceller M., Sumoy L.; Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.

RT [2]

RP SEQUENCE FROM N.A.

RA Auftray C., Ansoorge W., Ballabio A., Estivill X., Gibson K., Lehnach H., Pousika A., Lundberg J.; "The European IMAGE consortium for Integrated Molecular analysis of human gene transcripts.";

RT Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL389978; CAB97534.1; -

DR InterPro: IPR003006; -

DR InterPro: IPR003596; -

DR Pfam; PF00047; 1g.4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

DR SMART; SM00406; IGV; 1.

FT NON_TER 1

FT SEQUENCE 416 AA; 44786 MW; 8C41708BB8BA687 CRC64;

Query Match 22.0%; Score 547; DB 4; Length 416;
Best Local Similarity 33.3%; Pred. No. 8.5e-35;
Matches 144; Conservative 76; Mismatches 164; Indels 48; Gaps 19;

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DB 116 TWSESGONTARNPPSODASGDLTYTSSQLTLPATQCDDPKGSVCHVKHYTNPSODVTV 175
OY 212 DKLEPSPGISTINCPCKECKHCRAPNLEGGSVYFIPPNIKDYLMISLTPKVTGVV 271
DB 176 P-----CPVPPPPPC-CH-----PRLSIHPRALDELILGS-EANICTTLT 213
OY 272 DVEDDDPVOISMVFNVEVHTAQTOTHRDYNSTIRVSTLPIOHODMMSGEKCKVYN 331
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 GL-RDASGATFTWTPSSGK--SAVQGPPEKDLGCYSVSVLPGCAQPMNHGFTCTAA 270
OY 332 NKRLPSPLETKISIKIGLVAPQVYILPPAPDLSRKD-VSLTCLVGVNPGDISVEMTS 390
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
271 HPELKTPTLTANIRK-SGNFTFPPVHLPLPPESEALANEVTLCLARGFSPKVLVRLQ 329
OY 391 NGH--TEENYKQDAPVLD-SDG--SYFIYSKLMNKTSSKMEKTDSESCNVHREGKLNKYLK 445
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
330 GSQELPREKLTWASROEBSQGITTFVAVTSLVAAEDMKGDTFSCMVGHEALPLAFIQ 389
OY 446 KTISRSPGKGH 457
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 390 KTIDRLAKRPTH 401

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RESULT 3

ID Q9QXF0 PRELIMINARY: PRT: 117 AA.

AC Q9QXF0; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)

DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

ON [1]

RP SEQUENCE FROM N.A.

RA Clemens A., Rademakers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ225171; CAB65236.1; -

DR InterPro: IPR003006; -

DR InterPro: IPR003596; -

DR Pfam; PF00047; 1g.1.

DR SMART; SM00406; IGV; 1.

FT NON_TER 1

FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47B4C CRC64;

Query Match 19.3%; Score 480.5; DB 11; Length 117;
Best Local Similarity 78.8%; Pred. No. 2.7e-30;
Matches 93; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAW-specific monoclonal antibodies with chimeric
RT IgG2/g4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: U78801; AAD00293.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 118 AA; 13036 MW; 90EBC559D31ECAFC CRC64;

Query Match 16.1%; Score 401; DB 11; Length 118;
Best Local Similarity 65.3%; Pred. No. 4.3e-24;
Matches 77; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

QY 1 EVOLQSGELVPGASVMISCTSAVTETENTVHWKOSHGSELMWIGINPYGSGIP 60
DB 1 QVQVQSGAELAPWASVKLSCKASGYNFNSYMWKQKRGGLMIGAITPGDDTSY 60
QY 61 SPFFKRAITLVDSSTAYMELRLTSEDSAVYCARAGAYFPYWGQTTLVSS 118
DB 61 TQFRKRAITLVDSSTAYMELRLTSEDSAVYCARAGAYFPYWGQTTLVSS 118

RESULT 8
ID 09JL81 PRELIMINARY; PRT; 114 AA.

AC 09JL81;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Lao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206025; AAF69323.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 114 AA; 12829 MW; 40A885FDE6BA56F8 CRC64;

Query Match 15.5%; Score 385; DB 11; Length 114;
Best Local Similarity 66.7%; Pred. No. 7.3e-23;
Matches 76; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

QY 9 PELVKGASVMISCTSAVTETENTVHWKOSHGSELMWIGINPYGSGIPKFKGA 68
DB 1 POLVKGASVKTICKASGYSFYSYMWKQKRGGLMIGAITPGDDTSRLNKKKKA 60
QY 69 TLTVDKSSSTAYMELRLTSEDSAVYCARAGAYFPYWGQTTLVSS 118

DB 61 TLTVDKSSSTAYMELRLTSEDSAVYCARAGAYFPYWGQTTLVSS 114

RESULT 9

ID 09JL77 PRELIMINARY; PRT; 110 AA.

AC 09JL77;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2;
RA Malkiel S., Lao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206025; AAF69327.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 110 AA; 12138 MW; 2EDEB1BF5862C9AF CRC64;

Query Match 15.2%; Score 379; DB 11; Length 110;
Best Local Similarity 65.7%; Pred. No. 2.1e-22;
Matches 71; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 11 LVKPGASVMISCTSAVTETENTVHWKOSHGSELMWIGINPYGSGIPSPFKKATL 70
DB 3 LVKPGASVKTICKASGYFTSSYMWKQKRGGLMIGAITPGDDTSYNEKFKKATL 62
QY 71 TVDKSSSTAYMELRLTSEDSAVYCARAGAYFPYWGQTTLVSS 118
DB 63 TVDTSSSTAYVLDLSTSEDSAVYCARAGAYFPYWGQTTLVSS 110

RESULT 10

ID 090544 PRELIMINARY; PRT; 684 AA.

AC 090544;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE NOVEL ANTIGEN RECEPTOR PRECURSOR.
OS Gingivomastoma citrarium (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Orectolobiformes;
OX Gingivomastomidae; Gingivomastoma.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE=95183140; PubMed=7877689;
RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks."
RL Nature 374:168-173(1995).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: U18701; AAB48195.1; -
DR HSPF; P01857; 1PCL.
DR InterPro: IPR003006; -
DR InterPro: IPR003597; -

DR Pfam; PF00047; Ig; 6.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 DR SMART; SM00407; IG1; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.
 SO SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6D6D CRC64;

Query Match 15.08; Score 372.5; DB 13; Length 684;
 Best Local Similarity 23.68; Pred. No. 6.6e-21;
 Matches 130; Conservative 88; Mismatches 205; Indels 129; Gaps 23;

QY 2 VOIQSGPELVKPGASVMISCRSATFTENTVHM-----VQSGIGE- 43
 DB 145 VSLHSAITEBORANRFVOLCLISGY-YPENIAVSQKNTKTITSGFATTSPTVSSND 203
 QY 44 ---SL-----EWIGGINPYGSGIFPKFKATLTVD---KSSSTAYMELRSTSED 90
 DB 204 SCASLAKVPIQEW-----SRGSVYGCQVSHSATSSNOKREIRSTEIANVLRDPYEE 256
 QY 91 ----SAVYIC-----ARRAGAYF-----DY 107
 DB 257 IMIDKSATLICEVLSTVSAGVYVSMVNGKVRNEGVMQEPFKMSGNOYLFTISRLTSVVE 316
 QY 108 WGGSTLTIVSS-----AKTTPSYVPLAPGCGD-TTGSSTVTLGCLVKG 149
 DB 317 WSGVEYTCCKKQDOSSTPVYKTRKARVEPTKPLRLPLPSPEIOTSTSATLTCLIRG 376
 QY 150 YFPESVTVTNWNSG--SLSSVYHFPALLOSL-YTMSSSVTVPSSTWPS-QTVTCVAHP 205
 DB 377 FYDPKVSVMQKDVSVSANTNFTALQDLFTSTSLNLTAVEKSGAKYCTIASHP 436
 QY 206 ASSTVDKLEPSPGISTINCPCKECHKCPADNLEGGSVFTFPNIKDVIMISLPK 265
 DB 437 PSOSTVVRVIR-----NOKVDCROT-----DISVSLKPPFEET-WTQGTAT 477
 QY 266 VTCVYVVDSEDDPDVOISWFPNNVEVHTAQOTHREDYNSIRVAVSLPIQHOVMGSGKE 325
 DB 478 IVCEI--VYSDLENIKVFQWQVNGERKKGVETQNPWMSGSKTVSVKLKVASMDSGTE 535
 QY 326 FKCVVNNKDLPSPIERTISKIK-GLVRAPQVYILPPAEOL-SKRDVSLFCLVYGFNPGD 383
 DB 536 YVCLVEDESLPTPKASIRKIRANVSQMPKRYLLHPSTDEIDTENSATLMCLANFPAE 595
 QY 384 ISVEWTSNGH-TEENYKDTAPVLDSDGSFYTSKLNNKTSKWEKTDSESCNVRHEGLKNY 442
 DB 596 IYVGMMANDTLDDSGYRQYVDSEKSGSSPVTDRILRTAAEMNSDITYSCLVGHPISLRD 655
 QY 443 YLKTTISRPCK 454
 DB 656 LIRST-NKSNCK 666

RESULT 11
 Q9Y298 PRELIMINARY; PRT; 150 AA.
 AC Q9Y298;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ICG VH PROTEIN PRECURSOR (FRAGMENT).
 GN ICG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98322155; PubMed=9657749;
 RA Jacquemin M.G., Vander Elst L.P.L.;
 RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with an

RT Inhibitor."
 RL BLOD 92:496-506 (1998).
 CC -1- SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AJ224083; CAA11829.1; -.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT NON_TER 150 150
 SO SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 14.98; Score 371.5; DB 4; Length 150;
 Best Local Similarity 56.68; Pred. No. 1.2e-21;
 Matches 73; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
 QY 1 EVOIQSGPELVKPGASVMISCRSATFTENTVHMVKOSHGESLEWIGINPYGGSIF 60
 DB 20 QVOLVQSGAEYKPKGASVSKVSGYTLTLPVHMVQAGKGLWVGSFDPSSGSIT 79
 QY 61 SPKFKATLTVDRSSSTAYMELRSTSEDSAVYVCARRAGAYFEDYWGQSTLTIVSSAK 120
 DB 80 AREFGSGVTMTADSTDIAYMELSLSDPDAVYCA-VPPDPAFDIMGQGTMTVSSAS 138
 QY 121 TTPPSVYPL 129
 DB 139 TKGPSVEPL 147

RESULT 12
 Q9Y298 PRELIMINARY; PRT; 157 AA.
 AC Q9Y298;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE VH1 PROTEIN PRECURSOR (FRAGMENT).
 GN VH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,
 RA Bohnen H., Diehl V., Wolf J.;
 RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
 RT patient with mixed cellularity Hodgkin's disease is associated with
 RT somatic mutations within the untranslated regions of rearranged and
 RT class switch recombined Ig genes";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases
 CC -1- SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AJ005570; CAA06599.1; -.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT NON_TER 157 157
 SO SEQUENCE 157 AA; 17304 MW; 86986EDDA84D8B5 CRC64;

Query Match 14.98; Score 369.5; DB 4; Length 157;
 Best Local Similarity 51.98; Pred. No. 1.8e-21;
 Matches 70; Conservative 25; Mismatches 35; Indels 5; Gaps 2;
 QY 1 EVOIQSGPELVKPGASVMISCRSATFTENTVHMVKOSHGESLEWIGINPYGGSIF 60

Db	20	QVQLVQSGAEELKRRGASVKAKVCHKSTGYFETYYTHHWKQPRPGDGLBMMGGIGRVSSTMC	79
QY	61	SPKEKGATFLVDSKSSSTAYNELSLTSEDSAVYYCAR---RAGAYYFDYWGQGLTVL	116
Db	80	AEKFGGRLTMRNRTSTTVYWELSRLREFDPAVYFCGRGGRGFRSGNYN-GHMGQGTVEV	138
QY	117	SSAKTTPSPSYPLAP	131
Db	139	SSSSTKGSPSYEPLAP	153

RESULT	13			
ID	09GYZ2	PRELIMINARY;	PRT;	119 AA.
AC	09GYZ2;			
DT	01-MAR-2001 (TREMBlrel, 16, Created)			
DT	01-MAR-2001 (TREMBlrel, 16, Last sequence update)			
DT	01-MAR-2001 (TREMBlrel, 16, Last annotation update)			
DE	MONOCLONAL ANTI-IDIDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Schistosoma japonicum (Blood fluke).			
OC	Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;			
OC	Trematoda; Digenea; Strigeiida; Schistosomatoida; Schistosomatidae;			
OC	Schistosoma.			
OX	NCBI_TaxID=6182;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Song X.T., Peng Z.O., Guan X.H.;			
RT	"Amplification, cloning and sequence analysis of the heavy chain			
RT	variable region gene of monoclonal anti-idiotypic antibody NP30 of			
RL	Schistosoma japonicum."			
DR	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
EMBL:	AF282622; AAC01452.1; .			
FT	NON_TER	1	1	
FT	NON_TER	119	119	
SQ	SEQUENCE	119 AA;	13567 MW;	BA893873FDSFACAB CRC64;

Query Match	14.7%	Score 366.5;	DB 5;	Length 119;
Best Local Similarity	60.5%	Pred. No. 2.2e-21;		
Matches	72;	Conservative 17;	Mismatches 29;	Indels 1;
				Gaps 1.

[illegible]

RESULT	14
090U192	
ID	
AC	090U192;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98271139; PubMed=9614934;
RA	Wu X., Liu B., Van der Werf P.L., Kalls N.N., Berney S.M.,
RA	Young D.C.;
RT	Myosin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.;
RL	clin. Immunol. Immunopathol. 87:184-192(1998).
CC	1.- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC	DOMAIN.		
DR	EMBL:	AF035022:	AAD56258.1; -.
DR	InterPro:	IPR003006:	-.
DR	InterPro:	IPR003596:	-.
DR	Pfam:	PF00047:	15; 1.
DR	SMART:	SM00406:	IGV; 1.
FT	NON_TER		
FT		124	1
SO	SEQUENCE	124 AA:	13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 14.6%; Score 364; DB 4; Length 124;
Best Local Similarity 56.3%; Pred. No. 3.6e-21;
Matches 71; Conservative 19; Mismatches 26; Indels 10; Gaps 2

[illegible]

RESULT	15			
Q9JL85				
ID	Q9JL85	PRELIMINARY;	PRT;	109 AA.
AC	Q9JL85;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)			
DE	ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RA	Malikci S., Liao L., Cunningham M.W., Diamond B.;			
RT	"Characterization of cross-reactive monoclonal anti-myosin/anti-n-			
RT	acetyl-glucosamine antibodies from mice with autoimmune myocarditis."			
RL	Submitted (NOV-1999) to the EMBL/Genbank/DBD databases.			
DR	EMBL; AF206021; AAF69319.1; -.			
DR	InterPro; IPR003006; -.			
DR	InterPro; IPR003596; -.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
FT	NON_TER	1		
FT	NON_TER	109	109	
Q0	SEQUENCE	109 AA;	11944 MW;	DFE615FE6CED4DE CRC64;

Query Match	14.48;	Score 358.5;	DB 11;	Length 109;
Best Local Similarity	63.38;	Pred. No. 8.1e-21;		
Matches	69;	Conservative	13;	Mismatches 26;
			Indels	1;
			Gaps	1;

[illegible]

Search completed: June 18, 2001, 15:34:08
Job time: 231 sec

